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ALKALINE BACILLUS AMYLASE

FIELD OF INVENTION

The present invention relates to amylases having improved washing performance in an alkaline detergent solution at low temperature.

5 BACKGROUND OF THE INVENTION

For a number of years α -amylase enzymes have been used for a variety of different purposes, the most important of which are starch liquefaction, textile desizing, starch modification in the paper and pulp industry, and for brewing and baking. A further use of α -amylases, which is becoming increasingly important is the removal of
10 starchy stains during washing with a detergent at alkaline pH.

Examples of commercial α -amylase products are Termamyl®, BAN® and Fungamyl®, all available from Novo Nordisk A/S, Denmark. These and similar products from other commercial sources have an acidic to a neutral pH optimum, typically in the range of from pH 5 to pH 7.5, and they do not display optimal activity in
15 detergent solutions at alkaline pH.

WO 95/26397 discloses an α -amylase from a *Bacillus* strain which has optimum activity at pH 8. WO 96/23873 describes variants of *Bacillus* amylases with improved performance under washing conditions.

US 5,147,796 describes an alkaline pullulanase having alpha-amylase
20 activity. Fig. 2b of the document shows optimum amylase activity at pH 8-8.5.

M. Takagi et al., J. Ferment. Bioeng., vol 81, No. 6, 557-559 (1996) describe an alkaliphilic alpha-amylase-pullulanase from *Bacillus* sp. The enzyme has optimum amylase activity at pH 9, but the activity drops rapidly at higher pH, and the activity at pH 10 is lower than at pH 7.

25 It is an object of the present invention to provide novel α -amylases with improved performance in alkaline solutions, especially in alkaline detergent solutions at pH around 9-11.

SUMMARY OF THE INVENTION

The present invention provides alpha-amylase which is:

- 30 a) a polypeptide produced by *Bacillus* sp. NCIMB 40916, or
b) a polypeptide having an amino acid sequence as shown in positions 1-501 of SEQ ID NO: 2, or
c) an analogue of the polypeptide defined in (a) or (b) which:
i) is at least 60 % homologous with said polypeptide, or
35 ii) is derived from said polypeptide by substitution, deletion and/or insertion of one or several amino acids.

In another aspect, the invention provides an α -amylase having one or more of the following characteristics:

- an activity at pH 10.5 which is at least two times higher than the activity at pH 7.3 when measured at 37°C.

5 •an activity at pH 9.5 which is at least 4 times higher than the activity at pH 7.3 when measured at 37°C.

- an optimum pH of about 9.5 when measured at 37°C.

- a thermostability such that it retains more than 90 % of its activity after 20 minutes incubation at 25°C in a solution of 3 g/l of a test detergent containing 20% STPP, 25% Na₂SO₄, 15% Na₂CO₃, 20% LAS, 5% C12-C15 alcohol ethoxylate, 10 5% Na₂Si₂O₅, 0.3% NaCl at pH 10.5 and 6 degrees German hardness, and retains less than 90 % of its activity after 20 minutes incubation at 30°C in the same solution.

- a molecular weight of about 55 kDa as determined by SDS-PAGE.

15 •an iso-electric point of about 5 as determined by isoelectric focusing.

The invention also provides an isolated DNA sequence which encodes an alpha-amylase, wherein the alpha-amylase is that described above, or wherein the DNA sequence comprises:

- 20 a) the DNA sequence shown in positions 94- 1596 of SEQ ID NO: 1, or
 b) an analogue of the DNA sequence defined in a) which
 i) is at least 60 % homologous with said DNA sequence, or
 ii) hybridizes with said DNA sequence at ? °C.

Other aspects of the invention provide a recombinant expression vector comprising the DNA sequence, and a cell transformed with the DNA sequence or 25 the recombinant expression vector.

The invention also provides a method for producing an alpha-amylase by cultivating the cell and a detergent composition comprising said alpha-amylase.

BRIEF DESCRIPTION OF DRAWINGS

30 The present invention is further illustrated with reference to the accompanying drawings, in which:

Fig. 1 shows a pH activity profile of the amylase from NCIMB 40916 compared to two prior-art amylases (SP722 and Termamyl). (= Fig. 1 of "Fremst~1.doc")

35 Fig. 2 shows a temperature activity profile of the amylase from NCIMB 40916. (= Fig. 2 of "Fremst~1.doc")

Fig. 3 shows the stability of the amylase from NCIMB 40916 after incubation at various temperatures. (= Fig. 3 of "Fremst~1.doc")

Fig. 4 shows the cloning vector pSJ1678 described in Example 1. (= Fig. 1 of BC7_gene.doc)

Figs. 5 and 6 show results of washing tests described in Example 4. (from Bc7.xls)

5 DETAILED DESCRIPTION OF THE INVENTION

Microbial source

The alpha-amylase of the invention may be derived from a strain of *Bacillus*. A preferred strain is *Bacillus sp.* NCIMB 40916. This strain was deposited on 28 January 1998 (28.01.98) by the inventors under the terms of the Budapest
10 Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure at the National Collections of Industrial and Marine Bacteria Limited (NCIMB), 23 St. Machar Drive, Aberdeen AB2 1RY, Scotland, United Kingdom.

Production of alpha-amylase

15 The alpha-amylase of the invention can be produced by cultivating a suitable amylase-producing strain of *Bacillus* or the transformed host cell of the invention in a suitable nutrient medium, and recovering the alpha-amylase from the culture medium.

The medium used to cultivate the cells may be any conventional medium
20 suitable for growing the host cell in question and obtaining expression of the α -amylase of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. as described in catalogues of the American Type Culture Collection).

The α -amylase secreted from the host cells may conveniently be
25 recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

30 Properties of alpha-amylase

A preferred alpha-amylase is derived from *Bacillus sp.* NCIMB 40916. It can be produced as described in the examples. The amino acid sequence of the amylase and of the DNA encoding it are shown in SEQ ID NO: 1 and 2. The following characteristics were found for an amylase of the invention (purified
35 alpha-amylase from NCIMB 40916):

A molecular weight of approximately 55 kDa as determined by SDS-PAGE using a Novex, 4-25% gradient gel.

A pI of approximately 5 was determined by isoelectric focusing (Ampholine PAG, pH 3.5-9.5).

5 A pH-activity curve is shown in Fig. 1, taking the activity at pH 7.3 as 100%. It was determined using the Phadebas assay using 50 mM Britten-Robinson buffer adjusted to various pH-values. For reference, the pH profiles of two prior-art *Bacillus* amylases (Termamyl derived from *B. licheniformis* and SP722 produced according to WO 95/26397) were measured under the same conditions
10 are also shown in Figure 1. Figure 1 shows that the amylase of the invention has about 10 times higher activity than the two prior-art amylases at pH 9.5. Fig. 1 also shows that the optimum activity is about pH 9.5.

A temperature-activity curve was measured using the Phadebas assay at various temperatures with 50 mM Britten-Robinson buffer adjusted to pH 9.5. The
15 results are shown in Fig. 2. It is seen from Fig. 2 that the amylase of the invention has optimum activity at about 55°C.

Stability of the amylase was measured at pH 10.5 (50 mM CAPS) at 22, 37, 45, 55 and 65 °C after 30 minutes incubation. The enzyme was diluted to 40 NU/ml in buffer and 25 microlitre sample was incubated at the respective
20 temperatures. After 30 minutes, the samples was chilled on ice and residual activity was determined. A stability profile of the amylase of the invention and a prior-art amylase (SP722) is shown in Figure 3.

Stability was tested by incubating 40 NU/ml of amylase in a solution of 3 g/l of the A/P model detergent described above, at pH 10.5 and 6°dH (German
25 hardness, Ca:Mg 2:1). After the incubation, the residual activity was measured by Phadebas at pH 7.3. The results were 95 % residual activity after incubation at 25°C, and 87 % at 30°C.

Homology of polypeptide and DNA sequence

The amino acid sequence homology may be determined as the degree of
30 identity between the two sequences indicating a derivation of the first sequence from the second. The homology may suitably be determined by means of computer programs known in the art. Thus, FASTA provided in GCG version 8 (Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453) may be used with the following settings: Scoring matrix: GenRunData:blosum50.cmp,
35 Variable pamfactor used Gap creation penalty: 12, Gap extension penalty: 2. Alternatively, Gap from GCG version 9 may be used with a translated version 8 peptide scoring matrix, a gap creation penalty of 30, a gap extension penalty of 1 using ntol's matrix (<http://plasmid/~bioweb/matrix/>) without end gap penalty.

The amino acid sequence exhibits a degree of identity preferably of at least 60%, preferably at least 70%, more preferably at least 80%, especially at least 90% or at least 95%, with the amino acid sequence shown in SEQ ID NO: 2.

The DNA sequence homology may be determined as the degree of identity
5 between the two sequences indicating a derivation of the first sequence from the second. The homology may suitably be determined by means of computer programs known in the art such as GAP provided in the GCG program package (described above). Thus, Gap GCGv8 may be used with the following default parameters: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, default
10 scoring matrix. GAP uses the method of Needleman/Wunsch/Sellers to make alignments.

The DNA construct of the present invention comprises a DNA sequence exhibiting a degree of identity preferably of at least 60%, preferably at least 70%, more preferably at least 80%, especially at least 90% or at least 95%, with the
15 amino acid sequence shown in SEQ ID NO: 2.

A homology search of known sequences showed homologies for the sequences of the invention with a number of *Bacillus* amylases in the range 31-34 % on amino acid basis and 46-48 % on DNA basis, determined as described above.

20 Hybridization

The hybridization is used to indicate that a given DNA sequence is analogous to a nucleotide probe corresponding to SEQ ID NO: 1. The hybridization conditions are described in detail below.

Suitable conditions for determining hybridization between a nucleotide
25 probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5 x SSC (standard saline citrate) for 10 min, and prehybridization of the filter in a solution of 5 x SSC (Sambrook et al. 1989), 5 x Denhardt's solution (Sambrook et al. 1989), 0.5 % SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook et al.
30 1989), followed by hybridization in the same solution containing a random-primed (Feinberg, A. P. and Vogelstein, B. (1983) *Anal. Biochem.* 132:6-13), ³²P-dCTP-labeled (specific activity > 1 x 10⁹ cpm/µg) probe for 12 hours at approx. 45°C. The filter is then washed two times for 30 minutes in 2 x SSC, 0.5 % SDS at a temperature of at least 55°C, more preferably at least 60°C, more preferably at
35 least 65°C, even more preferably at least 70°C, especially at least 75°C.

Molecules to which the oligonucleotide probe hybridizes under these conditions are detected using a x-ray film.

Recombinant expression vector

The expression vector of the invention typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

5 The recombinant expression vector carrying the DNA sequence encoding the α -amylase of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, 10 e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

15 In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA 20 sequence encoding an α -amylase of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dagA* promoters, the promoters of the *Bacillus licheniformis* α -amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus Amyloliquefaciens* α -amylase (*amyQ*), the 25 promoters of the *Bacillus subtilis* *xylA* and *xylB* genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α -amylase, *A. niger* acid stable α -amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate 30 isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α -amylase of the invention. Termination and polyadenylation sequences may suitably be derived from the same 35 sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

While intracellular expression may be advantageous in some respects, e.g. when using certain bacteria as host cells, it is generally preferred that the expression is extracellular.

Procedures suitable for constructing vectors of the invention encoding an α -amylase, and containing the promoter, terminator and other elements, respectively, are well known to persons skilled in the art [cf., for instance, Sambrook et al. (1989)].

15 Host cells

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of the α -amylase of the invention. The cell may be transformed with the DNA construct of the invention encoding the amylase, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of bacterial host cells which, on cultivation, are capable of producing the enzyme of the invention are gram-positive bacteria such as strains of *Bacillus*, such as strains of *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. clausii*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. coagulans*, *B. circulans*, *B. lautus*, *B. megaterium* or *B. thuringiensis*, or strains of *Streptomyces*, such as *S. lividans* or *S. murinus*, or gram-negative bacteria such as *Escherichia coli*. The transformation of the bacteria may be effected by protoplast transformation, electroporation, conjugation, or by using competent cells in a manner known per se (cf. Sambrook et al., supra).

The yeast organism may favourably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

Industrial Applications

Owing to their activity at alkaline pH values, the α -amylases of the invention are well suited for use in a variety of industrial processes, in particular the enzyme finds potential applications as a component in detergents, e.g. laundry and hard surface cleaning detergent compositions, but it may also be useful in the production of sweeteners and ethanol from starch. Thus, it may be used in conventional starch-converting processes, such as liquefaction and saccharification processes described in US Patent No. 3,912,590 and EP patent publications Nos. 252,730 and 63,909.

The alkaline α -amylase of the invention may also be used in the production of lignocellulosic materials, such as pulp, paper and cardboard, from starch reinforced waste paper and cardboard, especially where repulping occurs at pH above 7 and where amylases can facilitate the disintegration of the waste material through degradation of the reinforcing starch. The α -amylase of the invention is especially useful in a process for producing a papermaking pulp from starch-coated printed paper. The process may be performed as described in WO 95/14807, comprising the following steps:

- a) disintegrating the paper to produce a pulp,
- b) treating with a starch-degrading enzyme before, during or after step a), and
- c) separating ink particles from the pulp after steps a) and b).

The α -amylases of the invention may also be very useful in modifying starch where enzymatically modified starch is used in papermaking together with alkaline fillers such as calcium carbonate, kaolin and clays. With the alkaline α -amylases of the invention it becomes possible to modify the starch in the presence of the filler thus allowing for a simpler integrated process.

The α -amylase of the invention may also be very useful in textile desizing. In the textile processing industry, α -amylases are traditionally used as auxiliaries in the desizing process to facilitate the removal of starch-containing size which has served as a protective coating on weft yarns during weaving. Complete removal of the size coating after weaving is important to ensure optimum results in the subsequent processes, in which the fabric is scoured, bleached and dyed.

Enzymatic starch break-down is preferred because it does not involve any harmful effect on the fiber material. In order to reduce processing cost and increase mill throughput, the desizing processing is sometimes combined with the scouring and bleaching steps. In such cases, non-enzymatic auxiliaries such as alkali or
5 oxidation agents are typically used to break down the starch, because traditional α -amylases are not very compatible with high pH levels and bleaching agents. The non-enzymatic breakdown of the starch size does lead to some fiber damage because of the rather aggressive chemicals used. Accordingly, it would be desirable to use the α -amylases of the invention as they have an improved
10 performance in alkaline solutions. The α -amylases may be used alone or in combination with a cellulase when desizing cellulose-containing fabric or textile.

The α -amylases of the invention may also be very useful in a beer-making process; the α -amylases will typically be added during the mashing process.

Detergent Compositions

15 According to the invention, the α -amylase may typically be a component of a detergent composition, e.g., a laundry detergent composition. As such, it may be included in the detergent composition in the form of a non-dusting granulate, a stabilized liquid, or a protected enzyme. Non-dusting granulates may be produced, e.g., as disclosed in US 4,106,991 and 4,661,452 (both to Novo Industri A/S) and may
20 optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molecular weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty
25 acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in patent GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Other enzyme stabilizers are well known in the art.
30 Protected enzymes may be prepared according to the method disclosed in EP 238,216.

The properties of the alpha-amylase of the invention make it particularly suitable for use in alkaline detergents, e.g. at pH 9.5-10.5, and for washing at low temperatures, e.g. 20-40°C.

35 The detergent composition of the invention may be in any convenient form, e.g. as powder, granules, paste or liquid. A liquid detergent may be aqueous, typically containing up to 70% water and 0-30% organic solvent, or non-aqueous.

The detergent composition comprises one or more surfactants, each of which may be anionic, nonionic, cationic, or amphoteric (zwitterionic). The detergent will usually contain 0-50% of anionic surfactant such as linear alkylbenzenesulfonate (LAS), alpha-olefinsulfonate (AOS), alkyl sulfate (fatty alcohol sulfate) (AS), alcohol ethoxysulfate (AEOS or AES), secondary alkanesulfonates (SAS), alpha-sulfo fatty acid methyl esters, alkyl- or alkenylsuccinic acid, or soap. It may also contain 0-40% of nonionic surfactant such as alcohol ethoxylate (AEO or AE), alcohol propoxylate, carboxylated alcohol ethoxylates, nonylphenol ethoxylate, alkylpolyglycoside, alkyl dimethylamine oxide, ethoxylated fatty acid monoethanolamide, fatty acid monoethanolamide, or polyhydroxy alkyl fatty acid amide (e.g. as described in WO 92/06154).

The detergent composition may additionally comprise one or more other enzymes, such as pullulanase, esterase, lipase, cutinase, protease, cellulase, peroxidase, or oxidase, e.g., laccase.

Normally the detergent contains 1-65% of a detergent builder or complexing agent such as zeolite, diphosphate, triphosphate, phosphonate, citrate, nitrilotriacetic acid (NTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTMPA), alkyl- or alkenylsuccinic acid, soluble silicates or layered silicates (e.g. SKS-6 from Hoechst).

The detergent builders may be subdivided into phosphorus-containing and non-phosphorous-containing types. Examples of phosphorus-containing inorganic alkaline detergent builders include the water-soluble salts, especially alkali metal pyrophosphates, orthophosphates, polyphosphates and phosphonates. Examples of non-phosphorus-containing inorganic builders include water-soluble alkali metal carbonates, borates and silicates as well as layered disilicates and the various types of water-insoluble crystalline or amorphous alumino silicates of which zeolites is the best known representative.

Examples of suitable organic builders include alkali metal, ammonium or substituted ammonium salts of succinates, malonates, fatty acid malonates, fatty acid sulphonates, carboxymethoxy succinates, polyacetates, carboxylates, polycarboxylates, aminopolycarboxylates and polyacetyl carboxylates. The detergent may also be unbuilt, i.e. essentially free of detergent builder.

The detergent may comprise one or more polymers. Examples are carboxymethylcellulose (CMC), poly(vinylpyrrolidone) (PVP), polyethyleneglycol (PEG), poly(vinyl alcohol) (PVA), polycarboxylates such as polyacrylates, polymaleates, maleic/acrylic acid copolymers and lauryl methacrylate/acrylic acid copolymers.

The detergent composition may contain bleaching agents of the chlorine/bromine-type or the oxygen-type. The bleaching agents may be coated or encapsulated.

Examples of inorganic chlorine/bromine-type bleaches are lithium, sodium
5 or calcium hypochlorite or hypobromite as well as chlorinated trisodium phosphate. Examples of organic chlorine/bromine-type bleaches are heterocyclic N-bromo and N-chloro imides such as trichloroisocyanuric, tribromoisocyanuric, dibromoisocyanuric and dichloroisocyanuric acids, and salts thereof with water solubilizing cations such as potassium and sodium. Hydantoin compounds are
10 also suitable. The bleaching system may also comprise peroxyacids of, e.g., the amide, imide, or sulfone type.

The oxygen-type bleach may be an inorganic persalt, preferably with a bleach activator, or a peroxy acid compound. Examples of inorganic persalts are alkali metal perborates, both tetrahydrates and monohydrates, alkali metal
15 percarbonates, persilicates and perphosphates. The activator may be tetraacetylenediamine (TAED) or nonanoyloxybenzenesulfonate (NOBS).

The enzymes of the detergent composition of the invention may be stabilized using conventional stabilizing agents, e.g. a polyol such as propylene glycol or glycerol, a sugar or sugar alcohol, lactic acid, boric acid, or a boric acid
20 derivative such as, e.g., an aromatic borate ester, and the composition may be formulated as described in, e.g., WO 92/19709 and WO 92/19708. The enzymes of the invention may also be stabilized by adding reversible enzyme inhibitors, e.g., of the protein type as described in EP 0 544 777 B1.

The detergent may also contain other conventional detergent ingredients
25 such as, e.g., fabric conditioners including clays, deflocculant material, foam boosters, foam depressors, suds suppressors, anti-corrosion agents, soil-suspending agents, anti-soil-redeposition agents, dyes, dehydrating agents, bactericides, optical brighteners, or perfume.

The pH (measured in aqueous solution at use concentration) will usually
30 be neutral or alkaline, e.g. in the range of 7-11.

More specifically, the α -amylase of the invention may be incorporated in any of the detergent formulations described in WO 96/23873.

The α -amylases of the invention may be incorporated in concentrations conventionally employed in detergents. It is at present contemplated that, in the
35 detergent composition of the invention, the α -amylase may be added in an amount corresponding to 0.00001-1 mg (calculated as pure enzyme protein) of α -amylase per liter of wash liquor.

The present invention is further illustrated in the following examples which are not intended to be in any way limiting to the scope of the invention as claimed.

EXAMPLES

Host organism:

Escherichia coli SJ2 is described in Diderichsen, B., Wedsted, U., Hedegaard, L., Jensen, B.R., Sjøholm, C. (1990) Journal of Bacteriology, Vol.172, No. 8, p. 4315-4321.

Plasmids:

The gene bank vector was pSJ1678 which is further disclosed in WO94/19454 which is hereby incorporated by reference.

The gene bank vector pSJ1678 is further disclosed in WO 94/19454 which is hereby incorporated by reference.

Model detergent:

A/P (Asia/Pacific) Model Detergent has the following composition: 20% STPP (sodium tripolyphosphate), 25% Na₂SO₄, 15% Na₂CO₃, 20% LAS (linear alkylbenzene sulfonate, Nansa 80S), 5% C₁₂-C₁₅ alcohol ethoxylate (Dobanol 25-7), 5% Na₂Si₂O₅, 0.3% NaCl.

Example 1

Cloning of alpha-amylase into *E. coli*

DNA was isolated from *Bacillus sp.* NCIMB 40916 by the method of Pitcher, D. G., Saunders, N. A., and Owen, R. J. (1989) Lett. Appl. Microbiol. 8, 151-156. Chromosomal DNA was partially digested with the restriction enzyme Sau3AI. The fragments were cloned into the BamHI site of the cloning vector pSJ1678, as shown in Figure 4 and transformed into *Escherichia coli* SJ2, thereby creating a gene library of *Bacillus sp.* NCIMB 40916.

This gene library was screened for alpha amylase activity and the strain showing alpha amylase activity was termed JA388. This strain which harbours the plasmid encoding the alpha amylase was termed pJA388 and was used for DNA sequencing.

Example 2

Sequencing of DNA and alpha-amylase

The Alpha amylase gene cloned in plasmid pJA388 was characterized by DNA sequencing by primer walking, using the Taq deoxyterminal cycle sequencing kit (Perkin Elmer, USA), fluorescent labeled terminators and appropriate oligonucleotides as primers.

Analysis of the sequence data was performed according to Devereux et al. (1984) Nucleic Acids Res. 12, 387-395. The sequence corresponds to the DNA

sequence shown in SEQ ID NO: 1. The predicted protein sequence of the alpha amylase including the signal peptide and the mature alpha amylase are presented in SEQ ID NO: 2. The deduced N-terminal sequence was verified by sequencing 34 amino acids at the N-terminal of the protein.

5 Example 3

Production of alpha-amylase

E. coli JA388 harboring plasmid pJA388 was cultivated over night in LB-broth containing chloramphenicol 10 µg/ml, 37 °C, 250 rpm. Cells were harvested from 2.7 l culture broth by centrifugation at 6000 rpm for 15 minutes. The
10 intracellular located amylase was released from the cells by using the following osmotic shock procedure:

1) Cells were resuspended and washed in 500 ml 10 mM Tris- HCl, pH 7.0 (EKV-buffer) followed by centrifugation.

2) Cells were resuspended in 75 ml 20% sucrose, 30 mM Tris-HCl pH 8, 1
15 mM EDTA and added Lysozyme to a concentration of 5 mg/ml.

3) The solution was incubated 15 min on ice followed by centrifugation. The majority of the amylase was now contained in the supernatant.

The supernatant was dialyzed overnight against 10 l in EKV-buffer with one buffer change to decrease the high concentration of sucrose. The solution
20 was filtered through a 0.45 µm membrane vacuum filter.

The enzyme solution was applied on a Pharmacia Q Sepharose column FF previously equilibrated in EKV-buffer, pH 7, and the column was washed with EKV-buffer. Bound proteins were eluted with a linear NaCl gradient from 0-500 mM over 10 column volumes. Amylase containing fractions were pooled and
25 dialyzed against EKV-buffer over night.

The solution was then applied on a Q Sepharose column FF previously equilibrated in EKV-buffer, pH 8, the column was washed with EKV-buffer, and the amylase was eluted with a linear NaCl gradient from 0-500 mM over 10 column volumes. Amylase containing fractions were pooled.

30 A Phenyl Superose column previously equilibrated in EKV-buffer, pH 8 containing 1 M ammonium sulfate was loaded with the enzyme solution added ammonium sulfate to a concentration of 1 M. Unbound material was washed out with the ammonium sulfate buffer and the column was eluted with a linear NaCl gradient from 1-0 M ammonium sulfate over 20 column volumes. Amylase
35 containing fractions were pooled.

The purified amylase was analyzed by SDS-PAGE and only one band was obtained after staining with Coomassie Blue.

Example 4**Washing test**

Washing performance was evaluated by washing soiled test swatches for 15 minutes at 25°C in a detergent solution with the alpha-amylase of the invention.

5 The detergent used was the A/P Model Detergent described above at 3 g/l having pH 10.5, or a commercial detergent from Malaysia (FAB Total from Colgate) at 3 g/l having a pH of approx. 9.7. The purified amylase of Example 3 was added to the detergent solution at the concentration indicated below. The test swatches were soiled with orange rice starch (CS-28 swatches available from
10 CFT, Center for Test Material, Holland).

After washing, the swatches were evaluated by measuring the remission at 460 nm. The results are expressed as ΔR = remission of the swatch washed with the alpha-amylase minus the remission of a swatch washed at the same conditions without the alpha-amylase.

Alpha-amylase concentration (mg enzyme protein / l)	ΔR Model detergent	ΔR Malaysian detergent
0 (reference)	= 0	= 0
0.1	0.9	1
0.2	1.9	1.3
0.5	3	2.4
1.5	4.1	4.3

15 The results are shown in Figures 5 and 6. The results demonstrate that the alpha-amylase of the invention is effective in both detergents at highly alkaline pH.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Novo Nordisk A/S
- (B) STREET: Novo Alle
- (C) CITY: Bagsvaerd
- (E) COUNTRY: Denmark
- (F) POSTAL CODE (ZIP): DK-2880
- (G) TELEPHONE: +45-4444-8888
- (H) TELEFAX: +45-4449-3256

(ii) TITLE OF INVENTION: Alkaline amylase

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus sp.
- (B) STRAIN: NCIMB 40916

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION:1..1596

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION:1..93

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:94..1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG CAA AAC ACA GCG AAA AAC TCC ATC TGG CAG AGG GTG CGC CAC AGC
48

Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser
-31 -30 -25 -20

GCC ATT GCC TTA TCC GCT CTC AGT TTA TCC TTT GGC CTG CAG GCC AGC
96

Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser
-15 -10 -5 1

GAG TTA CCA CAA ATT CCA CCA CAG CAG GTG AAC AAC ACC ATG TAC CAG
144

Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln
5 10 15

GCA TTT TAT TGG GAT GCC TAC CCT GGC CTT TGG GCC AAT TTA CCG GCC
192

Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala
20 25 30

ATG GCG GCC CCT TTG GCC GAG CGT GGC ATT ACC TCG ATG TGG TTG CCG
240

Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro
35 40 45

CCC GCC GCC AAA GGC ATG AAT GGT ACT TTC AGT GTC GGT TAC GAT GTA
288

Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val
50 55 60 65

TAC GAT TTC TGG GAT CTG GGC GAG TTT AAC CAA AAA GGC ACC ACC GCC
336

Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala
70 75 80

ACC CGT TAC GGT ACT CGT CAG CAG CTG CAA CAA GCA CTG AGT GCT CTG
384

Thr Arg Tyr Gly Thr Arg Gln Gln Leu Gln Gln Ala Leu Ser Ala Leu
85 90 95

GAC CAA CTG GGT ATT CAG GCC TAT TTT GAT GTG GTG TTT AAC CAC CGC
432

Asp Gln Leu Gly Ile Gln Ala Tyr Phe Asp Val Val Phe Asn His Arg
100 105 110

ATG GGC GCC GAT GCA CAG GAG AAT ATT CCT GGC TTT GGC CTG GCC TGG
480

Met Gly Ala Asp Ala Gln Glu Asn Ile Pro Gly Phe Gly Leu Ala Trp
115 120 125

ACC GAG TAT CAT CTG CAA GGT CGT CAG GCG CAT TAT ACC CAG CAA AAC
528

Thr Glu Tyr His Leu Gln Gly Arg Gln Ala His Tyr Thr Gln Gln Asn
130 135 140 145

TGG GGC TAC TTG TGG CAC GAC TTT GAC TGG AAC TGG ACC GCG TTT AAT
576

Trp Gly Tyr Leu Trp His Asp Phe Asp Trp Asn Trp Thr Ala Phe Asn
150 155 160

GGC TCC GAC AAT CAG CTC TAC CCC GGC AAA TGG TGG GGC AAT ACC TTC
624

Gly Ser Asp Asn Gln Leu Tyr Pro Gly Lys Trp Trp Gly Asn Thr Phe
165 170 175

CAC TTC CCT TAT TTG ATG GGT GAG GAT GTC GAT TAC AAC CGC TTT GAA
672

His Phe Pro Tyr Leu Met Gly Glu Asp Val Asp Tyr Asn Arg Phe Glu
180 185 190

GTG CAG CAG GAA ATG AAA GCC TGG GGC GAG TGG ATC ATC AAC AGC GTT
720

Val Gln Gln Glu Met Lys Ala Trp Gly Glu Trp Ile Ile Asn Ser Val
195 200 205

GGC TTT AGC GGC TTT CGG ATG GAT GCC ATC GCC CAT GTC GAT ACC GAT
768

Gly Phe Ser Gly Phe Arg Met Asp Ala Ile Ala His Val Asp Thr Asp
210 215 220 225

TTT ACC CGT GAC TGG ATC AAT CAC GTG CAG TGG GCC ACC AGT GAG GAT
816

Phe Thr Arg Asp Trp Ile Asn His Val Gln Trp Ala Thr Ser Glu Asp
230 235 240

GTG TTC TTT GTC GCT GAA GCC TGG GTC AGT GAT ATC AAC GGC TAT CTG
864

Val Phe Phe Val Ala Glu Ala Trp Val Ser Asp Ile Asn Gly Tyr Leu
245 250 255

GAT GCA GTC AAT ACG CCG CAT TTG CGC GCT TTT GAT TTC AAT TTG CGC
912

Asp Ala Val Asn Thr Pro His Leu Arg Ala Phe Asp Phe Asn Leu Arg
260 265 270

GAA GAC TTC GTT GCT TTA AGC AGC GGT AGC AAA GAC ATG CGT TGG TGG
960

Glu Asp Phe Val Ala Leu Ser Ser Gly Ser Lys Asp Met Arg Trp Trp
275 280 285

GGC GGT CTG GTC AAT AGC CAG CAC CGT GAT CGG GCG GTC ACT TTT GTC
1008

Gly Gly Leu Val Asn Ser Gln His Arg Asp Arg Ala Val Thr Phe Val
290 295 300 305

GAT AAC CAC GAT ACC AGC CGG GCC GGC AAC CCT TAT GGC ATG CCG CAG
1056

Asp Asn His Asp Thr Ser Arg Ala Gly Asn Pro Tyr Gly Met Pro Gln
310 315 320

GTG ATC AAC TAC AAG AAC CAG GCC TAC GCT TAC ATT CTG TTG CGT GAG
1104

Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu
325 330 335

CAT GGG GTG CCG ACT GTG TTT GCC CGC GAT TAC GAC GAA TTT GGC ATG
1152

His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met
340 345 350

GCG CCA ACG CTG GAT AAA TTG ATT GAG GCG CGC CGC TAC TTT GCT TAT
1200

Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr
355 360 365

GGT CCT GGC CAT GAG TAC TCC GGC AAT ACC GAG GCC GTC TAC GCC TAT
1248

Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr
370 375 380 385

GTG CGC GAA GGG CTT AGC ACT GTG CCG GGT ACC GGT CTG GTG ATG CTG
1296

Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu
390 395 400

ATA TCG GGT CGA AAC TGG GGT GGT CAG CAG TCG TTC ACC ATC AAC AGC
1344

Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser
405 410 415

CAC CAG CCG AAT ACC ACC TTT TAC GAT TAT ACC GGC AAT GTT AGC GGC
1392

His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly

420 425 430

ACG GTG ACC ACC AAT GCG CAG GGC TAT GGC AGC TTC CCG GTC ACT ATG
1440
Thr Val Thr Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met
435 440 445

ACG GAA AGT ACC GGT TGG TCA GTC TTG GGT ACC ACA ATC CAA TGG TGG
1488
Thr Glu Ser Thr Gly Trp Ser Val Leu Gly Thr Thr Ile Gln Trp Trp
450 455 460 465

CAC TCA GCC GGG ATC CAT TAC CCT GCG GAT GAC CAA GGA TGT TGG CTA
1536
His Ser Ala Gly Ile His Tyr Pro Ala Asp Asp Gln Gly Cys Trp Leu
470 475 480

TGG CTT TTC GTT GTT CTT CAC CGG CAG CAG TGC GGA ACT GAC CAA CTG
1584
Trp Leu Phe Val Val Leu His Arg Gln Gln Cys Gly Thr Asp Gln Leu
485 490 495

GGG CGG CGG TAT TGA
1599
Gly Arg Arg Tyr
500

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser
-31 -30 -25 -20

Ala	Ile	Ala	Leu	Ser	Ala	Leu	Ser	Leu	Ser	Phe	Gly	Leu	Gln	Ala	Ser	-15	-10	-5	1
Glu	Leu	Pro	Gln	Ile	Pro	Pro	Gln	Gln	Val	Asn	Asn	Thr	Met	Tyr	Gln	5	10	15	
Ala	Phe	Tyr	Trp	Asp	Ala	Tyr	Pro	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Ala	20	25	30	
Met	Ala	Ala	Pro	Leu	Ala	Glu	Arg	Gly	Ile	Thr	Ser	Met	Trp	Leu	Pro	35	40	45	
Pro	Ala	Ala	Lys	Gly	Met	Asn	Gly	Thr	Phe	Ser	Val	Gly	Tyr	Asp	Val	50	55	60	65
Tyr	Asp	Phe	Trp	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Thr	Ala	70	75	80	
Thr	Arg	Tyr	Gly	Thr	Arg	Gln	Gln	Leu	Gln	Gln	Ala	Leu	Ser	Ala	Leu	85	90	95	
Asp	Gln	Leu	Gly	Ile	Gln	Ala	Tyr	Phe	Asp	Val	Val	Phe	Asn	His	Arg	100	105	110	
Met	Gly	Ala	Asp	Ala	Gln	Glu	Asn	Ile	Pro	Gly	Phe	Gly	Leu	Ala	Trp	115	120	125	
Thr	Glu	Tyr	His	Leu	Gln	Gly	Arg	Gln	Ala	His	Tyr	Thr	Gln	Gln	Asn	130	135	140	145
Trp	Gly	Tyr	Leu	Trp	His	Asp	Phe	Asp	Trp	Asn	Trp	Thr	Ala	Phe	Asn	150	155	160	
Gly	Ser	Asp	Asn	Gln	Leu	Tyr	Pro	Gly	Lys	Trp	Trp	Gly	Asn	Thr	Phe	165	170	175	
His	Phe	Pro	Tyr	Leu	Met	Gly	Glu	Asp	Val	Asp	Tyr	Asn	Arg	Phe	Glu	180	185	190	

Val Gln Gln Glu Met Lys Ala Trp Gly Glu Trp Ile Ile Asn Ser Val
195 200 205

Gly Phe Ser Gly Phe Arg Met Asp Ala Ile Ala His Val Asp Thr Asp
210 215 220 225

Phe Thr Arg Asp Trp Ile Asn His Val Gln Trp Ala Thr Ser Glu Asp
230 235 240

Val Phe Phe Val Ala Glu Ala Trp Val Ser Asp Ile Asn Gly Tyr Leu
245 250 255

Asp Ala Val Asn Thr Pro His Leu Arg Ala Phe Asp Phe Asn Leu Arg
260 265 270

Glu Asp Phe Val Ala Leu Ser Ser Gly Ser Lys Asp Met Arg Trp Trp
275 280 285

Gly Gly Leu Val Asn Ser Gln His Arg Asp Arg Ala Val Thr Phe Val
290 295 300 305

Asp Asn His Asp Thr Ser Arg Ala Gly Asn Pro Tyr Gly Met Pro Gln
310 315 320

Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu
325 330 335

His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met
340 345 350

Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr
355 360 365

Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr
370 375 380 385

Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu
390 395 400

Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser
405 410 415

His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly
420 425 430

Thr Val Thr Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met
435 440 445

Thr Glu Ser Thr Gly Trp Ser Val Leu Gly Thr Thr Ile Gln Trp Trp
450 455 460 465

His Ser Ala Gly Ile His Tyr Pro Ala Asp Asp Gln Gly Cys Trp Leu
470 475 480

Trp Leu Phe Val Val Leu His Arg Gln Gln Cys Gly Thr Asp Gln Leu
485 490 495

Gly Arg Arg Tyr
500

CLAIMS

1. An alpha-amylase which is:
 - a) a polypeptide produced by *Bacillus* sp. NCIMB 40916, or
 - b) a polypeptide having an amino acid sequence as shown in positions
5 1-501 of SEQ ID NO: 2, or
 - c) an analogue of the polypeptide defined in (a) or (b) which:
 - i) is at least 60 % homologous with said polypeptide, or
 - ii) is derived from said polypeptide by substitution, deletion and/or insertion of one or more amino acids.
- 10 2. An alpha-amylase which has an activity at pH 10.5 which is at least two times higher than the activity at pH 7.3 when measured at 37°C.
3. An alpha-amylase which has an activity at pH 9.5 which is at least 4 times higher than the activity at pH 7.3 when measured at 37°C.
- 15 4. An alpha-amylase which has an optimum pH of about 9.5 when measured at 37°C.
5. The alpha-amylase of any preceding claim which is from a strain of *Bacillus*, preferably *Bacillus* sp. NCIMB 40916.
6. The alpha-amylase of any preceding claim which retains more than 90 % of its activity after 20 minutes incubation at 25°C in a solution of 3 g/l of a test
20 detergent containing 20% STPP, 25% Na₂SO₄, 15% Na₂CO₃, 20% LAS, 5% C12-C15 alcohol ethoxylate, 5% Na₂Si₂O₅, 0.3% NaCl at pH 10.5 and 6 degrees German hardness, and retains less than 90 % of its activity after 20 minutes incubation at 30°C in the same solution.
7. The alpha-amylase of any preceding claim which has a molecular weight of
25 about 55 kDa as determined by SDS-PAGE.
8. The alpha-amylase of any preceding claim which has an iso-electric point of about 5 as determined by isoelectric focusing.
9. The alpha-amylase of any preceding claim in the form of a detergent additive which is a non-dusting granulate or a stabilized liquid.

10. An isolated DNA sequence which encodes the alpha-amylase of any of preceding claim.
11. An isolated DNA sequence which encodes an alpha-amylase and comprises:
- 5 a) the DNA sequence shown in positions 94- 1596 of SEQ ID NO: 1, or
 b) an analogue of the DNA sequence defined in a) which
 i) is at least 60 % homologous with said DNA sequence, or
 ii) hybridizes with said DNA sequence at ? °C.
12. The DNA sequence according to claim 10 or 11, which is from a bacterium,
10 preferably from *Bacillus*, most preferably from the strain NCIMB 40916.
13. A recombinant expression vector comprising the DNA sequence according to any of claims 10-12.
14. A cell transformed with the DNA sequence according to any of claims 10-12 or the recombinant expression vector according to claim 13.
- 15 15. The cell according to claim 14, which is a prokaryotic cell, in particular a bacterial cell or an endogenous cell from which said DNA sequence originates.
16. The cell according to claim 15, wherein the cell belongs to *Bacillus* or *Escherichia*, preferably *E. coli*.
17. A method of producing an alpha-amylase, comprising cultivating a cell
20 according to any of claims 14-16 under conditions permitting the production of the alpha-amylase, and recovering the alpha-amylase from the culture.
18. A method for producing the alpha-amylase of any of the preceding claims, comprising cultivating an amylase-producing strain of *Bacillus* in a suitable nutrient medium, and recovering the alpha-amylase from the culture medium.
- 25 19. A detergent composition comprising the alpha-amylase of any of claims 1-9 and a surfactant.
20. The detergent composition of the preceding claim which has a pH of 8.5-11 in aqueous solution, preferably pH 9-10.5

21. The detergent composition of claim 19 or 20 which is a laundry detergent.

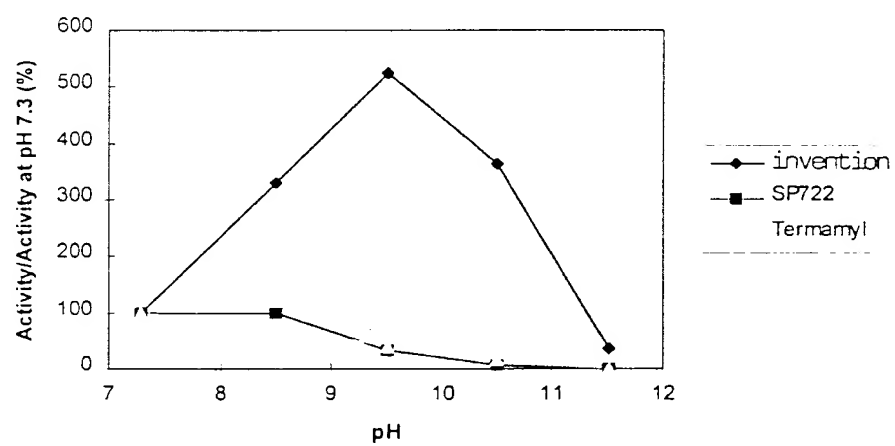


Fig. 1

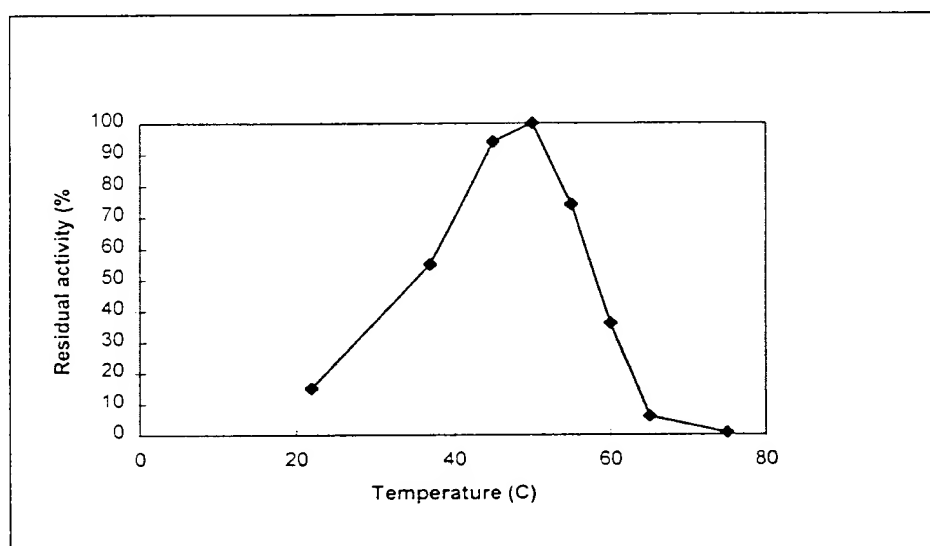


Fig. 2

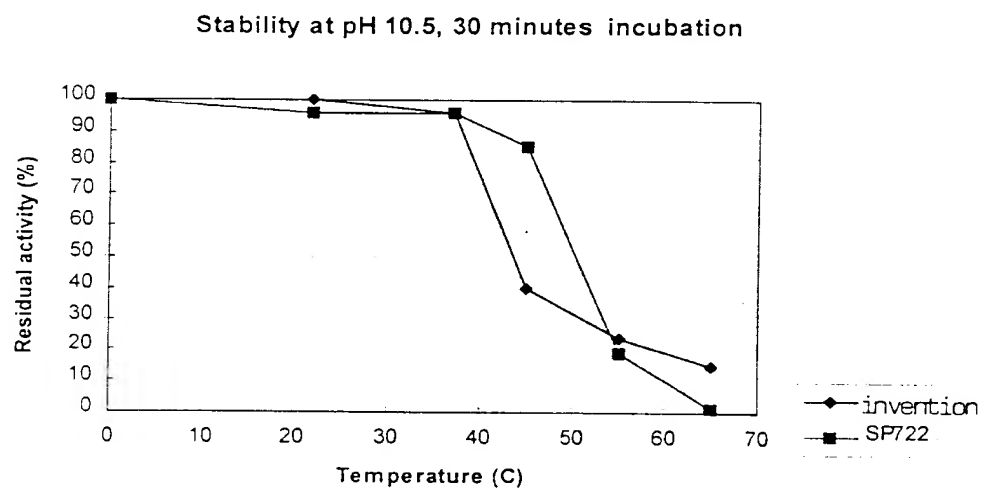


Fig. 3

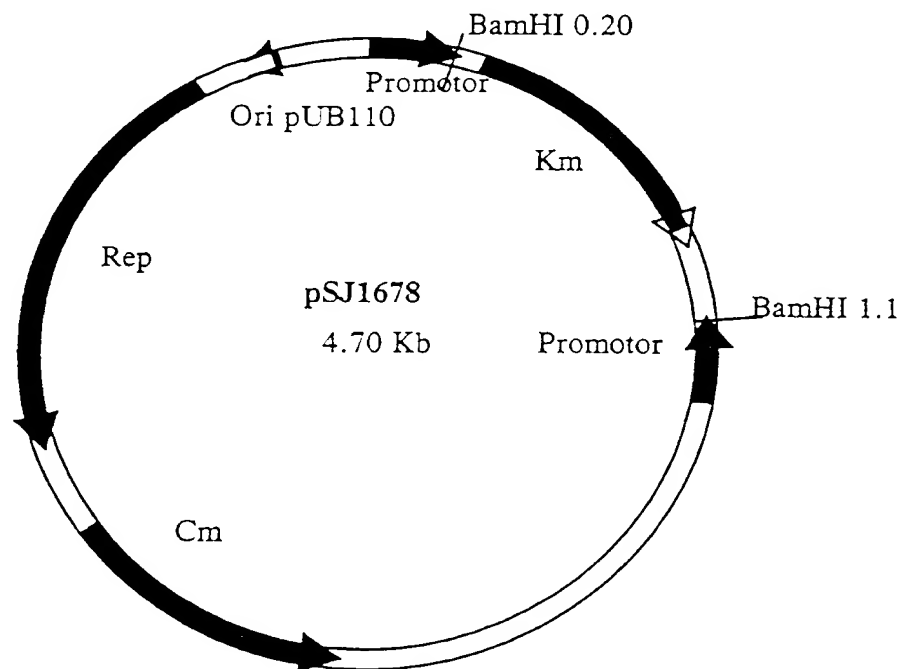


Fig. 4

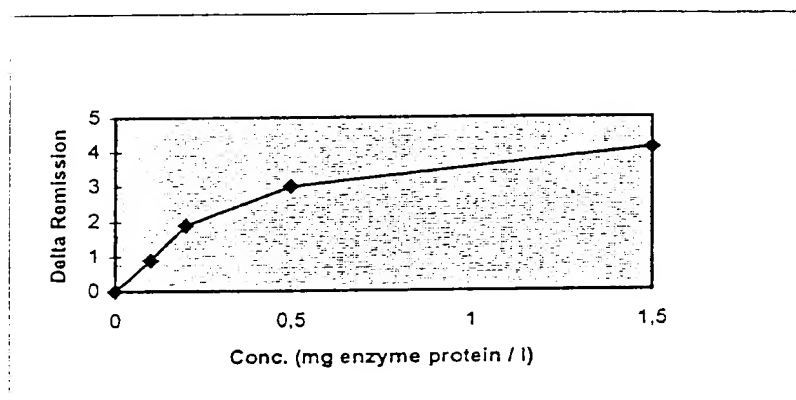


Fig. 5

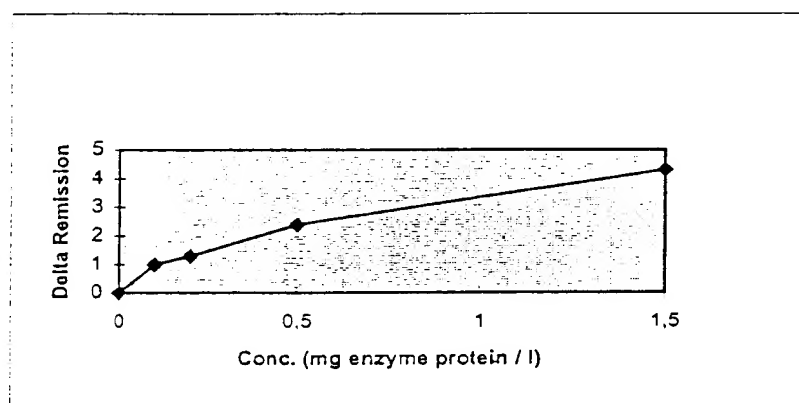


Fig. 6